

## SEQUENCE PROTOCOL

&lt;110&gt; Degussa AG

5 &lt;120&gt; Nucleotide sequences which code for the ilvE gene

&lt;130&gt; 000759 BT

&lt;140&gt;

&lt;141&gt;

&lt;160&gt; 2

&lt;170&gt; PatentIn Ver. 2.1

15 &lt;210&gt; 1

&lt;211&gt; 1453

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

20 &lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (221)..(1321)

&lt;223&gt; ilvE gene

25 &lt;400&gt; 1

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30 ccttagccatt cctcaaaaacc gtgagacgaa attggctatt catccccataa aatggggctg 180

actagtgtat ctgtcaggta gcagggtgtac cttaaaatcc atg acg tca tta gag 235  
Met Thr Ser Leu Glu 5  
1ttc aca gta acc cgt acc gaa aat ccg acg tca ccc gat cgt ctg aag 283  
Phe Thr Val Thr Arg Thr Glu Asn Pro Thr Ser Pro Asp Arg Leu Lys  
10 15 2040 gaa att ctt gcc gca ccg aag ttc ggt aag ttc ttc acc gac cac atg 331  
Glu Ile Leu Ala Ala Pro Lys Phe Gly Lys Phe Phe Thr Asp His Met  
25 30 3545 gtg acc att gac tgg aac gag tcg gaa ggc tgg cac aac gcc caa tta 379  
Val Thr Ile Asp Trp Asn Glu Ser Gly Trp His Asn Ala Gln Leu  
40 45 5050 gtg cca tac gcg ccg att cct atg gat cct gcc acc acc gta ttc cac 427  
Val Pro Tyr Ala Pro Ile Pro Met Asp Pro Ala Thr Thr Val Phe His  
55 60 65tac gga cag gca att ttt gag gga att aag gcc tac cgc cat tcg gac 475  
Tyr Gly Gln Ala Ile Phe Glu Gly Ile Lys Ala Tyr Arg His Ser Asp  
70 75 80 8555 gaa acc atc aag act ttc cgt cct gat gaa aac gcc gag cgt atg cag 523  
Glu Thr Ile Lys Thr Phe Arg Pro Asp Glu Asn Ala Glu Arg Met Gln  
90 95 100

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Arg Ser Ala Ala Arg Met Ala Met Pro Gln Leu Pro Thr Glu Asp Phe			
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5 att aaa gca ctt gaa ctg ctg gta gac gcg gat cag gat tgg gtt cct	619		
Ile Lys Ala Leu Glu Leu Leu Val Asp Ala Asp Gln Asp Trp Val Pro			
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10 gag tac ggc gga gaa gct tcc ctc tac ctg cgc cca ttc atg atc tcc	667		
Glu Tyr Gly Gly Glu Ala Ser Leu Tyr Leu Arg Pro Phe Met Ile Ser			
135	140	145	
15 acc gaa att ggc ttg ggt gtc agc cca gct gat gcc tac aag ttc ctg	715		
Thr Glu Ile Gly Leu Gly Val Ser Pro Ala Asp Ala Tyr Lys Phe Leu			
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20 gtc atc gca tcc cca gtc ggc gct tac ttc acc ggt gga atc aag cct	763		
Val Ile Ala Ser Pro Val Gly Ala Tyr Phe Thr Gly Gly Ile Lys Pro			
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25 gtt tcc gtc tgg ctg agc gaa gat tac gtc cgc gct gca ccc ggc gga	811		
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30 act ggt gac gcc aaa ttt gct ggc aac tac gcg gct tct ttg ctt gcc	859		
Thr Gly Asp Ala Lys Phe Ala Gly Asn Tyr Ala Ala Ser Leu Leu Ala			
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Gln Ser Gln Ala Ala Glu Lys Gly Cys Asp Gln Val Val Trp Leu Asp			
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40 gcc atc gag cac aag tac atc gaa gaa atg ggt ggc atg aac ctt ggg	955		
Ala Ile Glu His Lys Tyr Ile Glu Glu Met Gly Met Asn Leu Gly			
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45 ttc atc tac cgc aac ggc gac caa gtc aag cta gtc acc cct gaa ctt	1003		
Phe Ile Tyr Arg Asn Gly Asp Gln Val Lys Leu Val Thr Pro Glu Leu			
250	255	260	
50 tcc ggc tca cta ctt cca ggc atc acc cgc aag tca ctt cta caa gta	1051		
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55 gca cgc gac ttg gga tac gaa gta gaa gag cga aag atc acc acc acc	1099		
Ala Arg Asp Leu Gly Tyr Glu Val Glu Arg Lys Ile Thr Thr Thr			
280	285	290	
60 gag ttg gaa gaa gac gca aag tct ggc gcc atg acc gag gca ttt gct	1147		
Glu Trp Glu Glu Asp Ala Lys Ser Gly Ala Met Thr Glu Ala Phe Ala			
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65 tgc ggt act gca gct gtt atc acc cct gtt ggc acc gtc aaa tca gct	1195		
Cys Gly Thr Ala Ala Val Ile Thr Pro Val Gly Thr Val Lys Ser Ala			
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70 cac ggc acc ttc gaa gtg aac aac aat gaa gtc gga gaa atc acg atg	1243		
His Gly Thr Phe Glu Val Asn Asn Asn Glu Val Gly Glu Ile Thr Met			
330	335	340	

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Lys Leu Arg Glu Thr Leu Thr Gly Ile Gln Gln Gly Asn Val Glu Asp	
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5 caa aac gga tgg ctt tac cca ctg gtt ggc taaatcaacc ggtttaaga	1341
Gln Asn Gly Trp Leu Tyr Pro Leu Val Gly	
360	365
10 ccccgctgca ttaaaacctg attatttgca gcgggggttt tgcttgaca agctcttatg	1401
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<213> Corynebacterium glutamicum	
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30	35
30 Phe Thr Asp His Met Val Thr Ile Asp Trp Asn Glu Ser Glu Gly Trp	
35	40
45	45
35 His Asn Ala Gln Leu Val Pro Tyr Ala Pro Ile Pro Met Asp Pro Ala	
50	55
60	
35 Thr Thr Val Phe His Tyr Gly Gln Ala Ile Phe Glu Gly Ile Lys Ala	
65	70
75	80
35 Tyr Arg His Ser Asp Glu Thr Ile Lys Thr Phe Arg Pro Asp Glu Asn	
85	90
95	
40 Ala Glu Arg Met Gln Arg Ser Ala Ala Arg Met Ala Met Pro Gln Leu	
100	105
110	
45 Pro Thr Glu Asp Phe Ile Lys Ala Leu Glu Leu Leu Val Asp Ala Asp	
115	120
125	
50 Gln Asp Trp Val Pro Glu Tyr Gly Gly Glu Ala Ser Leu Tyr Leu Arg	
130	135
140	
50 Pro Phe Met Ile Ser Thr Glu Ile Gly Leu Gly Val Ser Pro Ala Asp	
145	150
155	160
55 Ala Tyr Lys Phe Leu Val Ile Ala Ser Pro Val Gly Ala Tyr Phe Thr	
165	170
175	
Gly Gly Ile Lys Pro Val Ser Val Trp Leu Ser Glu Asp Tyr Val Arg	
180	185
190	
55 Ala Ala Pro Gly Gly Thr Gly Asp Ala Lys Phe Ala Gly Asn Tyr Ala	
195	200
205	

	Ala Ser Leu Leu Ala Gln Ser Gln Ala Ala Glu Lys Gly Cys Asp Gln			
210	215	220		
5	Val Val Trp Leu Asp Ala Ile Glu His Lys Tyr Ile Glu Glu Met Gly			
225	230	235	240	
	Gly Met Asn Leu Gly Phe Ile Tyr Arg Asn Gly Asp Gln Val Lys Leu			
	245	250	255	
10	Val Thr Pro Glu Leu Ser Gly Ser Leu Leu Pro Gly Ile Thr Arg Lys			
	260	265	270	
	Ser Leu Leu Gln Val Ala Arg Asp Leu Gly Tyr Glu Val Glu Glu Arg			
	275	280	285	
15	Lys Ile Thr Thr Thr Glu Trp Glu Glu Asp Ala Lys Ser Gly Ala Met			
	290	295	300	
20	Thr Glu Ala Phe Ala Cys Gly Thr Ala Ala Val Ile Thr Pro Val Gly			
	305	310	315	320
	Thr Val Lys Ser Ala His Gly Thr Phe Glu Val Asn Asn Asn Glu Val			
	325	330	335	
25	Gly Glu Ile Thr Met Lys Leu Arg Glu Thr Leu Thr Gly Ile Gln Gln			
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	Gly Asn Val Glu Asp Gln Asn Gly Trp Leu Tyr Pro Leu Val Gly			
	355	360	365	
30				